REMARKS

Claims 1-7 are pending in the present application.

The rejection of Claim 1 under 35 U.S.C. §102(e) over Hatada et al is obviated in part by amendment and traversed in part.

The Examiner has maintained his position that Hatada et al anticipates the claimed invention. The Examiner alleges that Claim 1 is to be interpreted as including many mutations over the sequence of SEQ ID NO: 1 so as to embrace SEQ ID NO: 2 defined in Hatada et al which has 97.5% homology to SEQ ID NO: 1 and contains the specific mutations at 226 (tyrosine) and 296 (valine). The Examiner's position is set forth on page 6 of the Office Action in which she alleges that "claim 1 is directed to "one or more residues" selected from the specific point mutations and the claim recites the open language of "having" which is equivalent to comprising, thus is not limited to the 7 positions recited in the claim. The disclosed 97.5% sequence identity to SEQ ID NO: 1 is over the full-length sequence and a result of the additional mutations, which are encompassed in the open language recited in the claim". This allegation by the Examiner is completely without merit and is a gross misinterpretation of the language of Claim 1.

Regardless of whether the transition term "having" is used, the simple fact is that Claim 1 *requires* that the sequence be SEQ ID NO: 1, with the possible recited mutations and only the possible recited mutations as the "one or more residues" language is qualified by the specifically defined Markush group.

Nonetheless, to address this ground of rejection, Applicants have amended Claim 1 to replace "having" with "consisting of". Therefore, Hatada et al fails to anticipate the

invention of amended Claim 1 since the sequences disclosed therein do not fall within the scope of present Claim 1.

Applicants request withdrawal of this ground of rejection.

The rejection of Claim 2 under 35 U.S.C. §112, first paragraph (written description - new matter), is respectfully traversed.

The Examiner has rejected Claim 2 as containing new matter. The Examiner alleges that the specification fails to provide support for the limitation of "98.1% homology." Applicants disagree with the Examiner.

Support for the amendment of Claim 2 is implicitly provided by the eight defined amino acid substitutions recited in original Claim 2 that occur in a 434 amino acid protein ((434-8)/434 * 100 = 98.1% homology) and would be understood to be embraced by the claimed disclosure when view together with the paragraph bridging pages 7 and 8. Indeed, there is no requirement that there be an explicit recitation of the limitation of 98.1% homology where the specification provides implicit support for the same. Therefore, this rejection is without merit and should be withdrawn.

Withdrawal of these grounds of rejection is requested.

The objection to Claim 1 (and Claim 2) is believed to be obviated by amendment.

The Examiner has objected to the language of Claim 1 (and Claim 2) and requested that for, clarity and precision, the end of Claim 1 and presumably Claim 2 be amended as follows: "(g) serine, and wherein said isolated alkaline protease has alkaline protease activity." Consistent with this recommendation, Applicants have made the appropriate amendment to the claims.

In view of the foregoing, Applicants request withdrawal of this ground of objection.

The objection to the Abstract is believed to have been obviated by amendment. The Examiner has requested that Applicants correct a typographical error in the Abstract. Applicants have made the appropriate amendment to address this criticism. As such, withdrawal of this ground of objection is requested.

Accordingly, Applicants submit that the present application is now in condition for allowance. Early notification of such action is earnestly solicited.

Respectfully submitted,

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